

Figure 1.

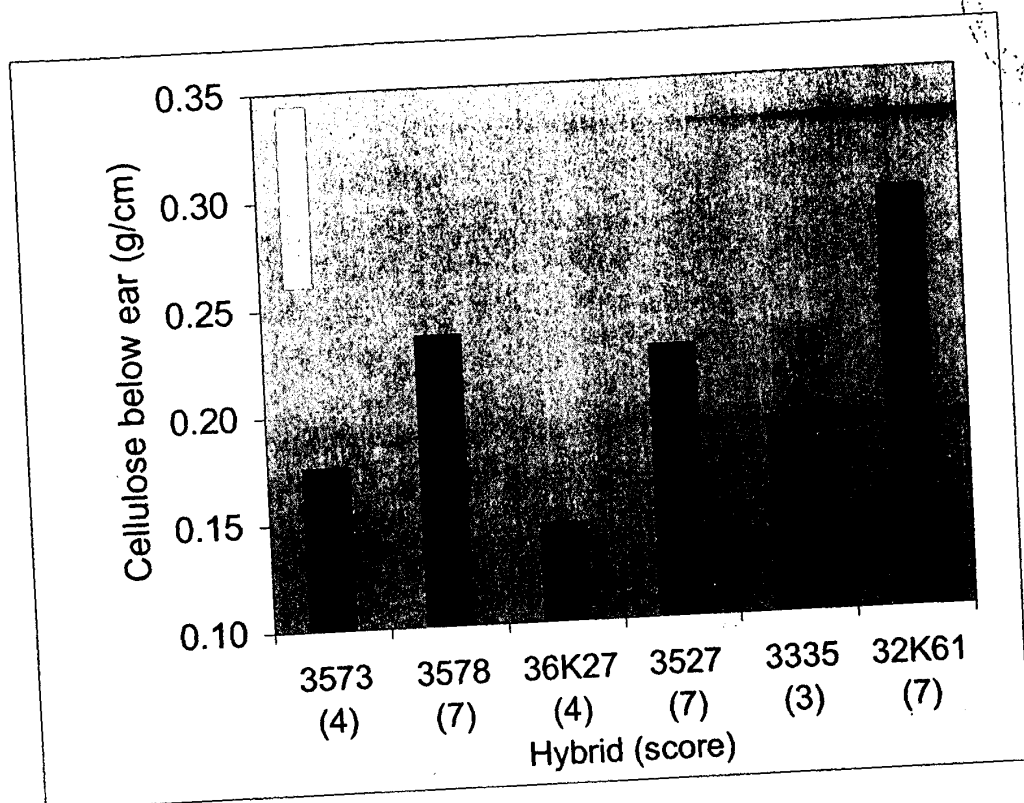


Figure 2

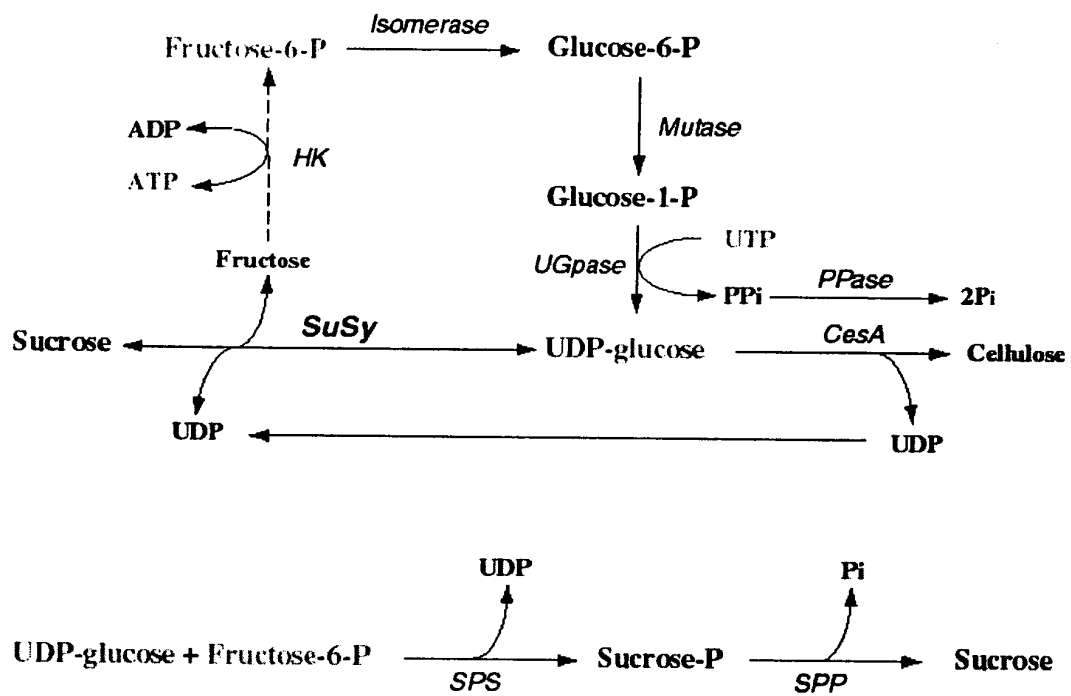


Figure 3.

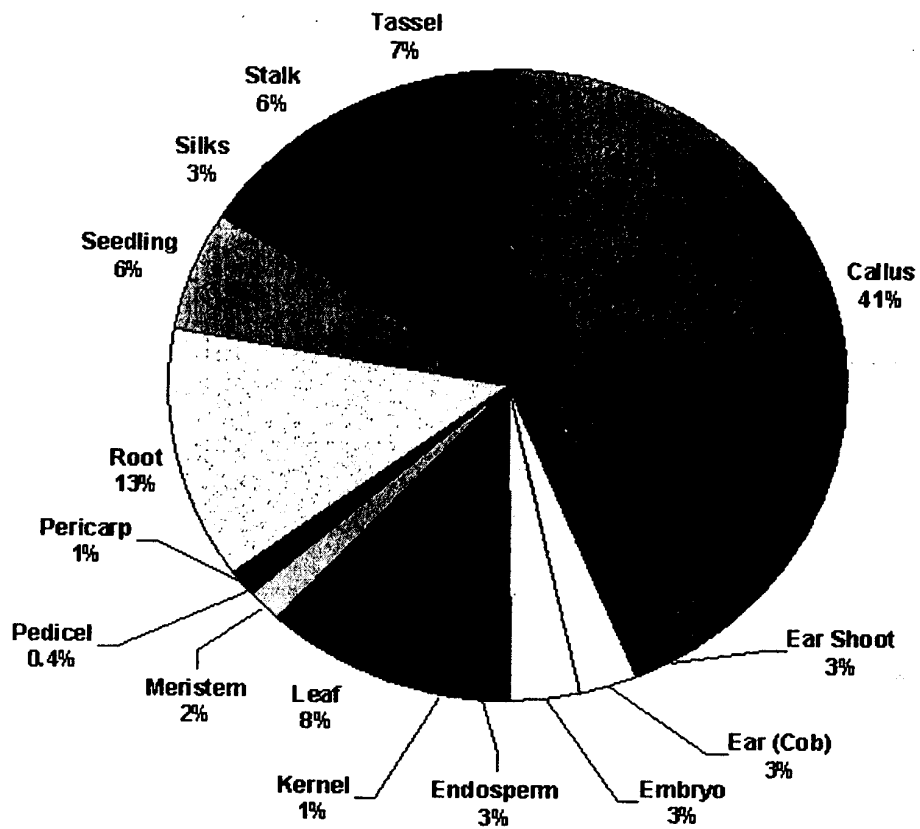
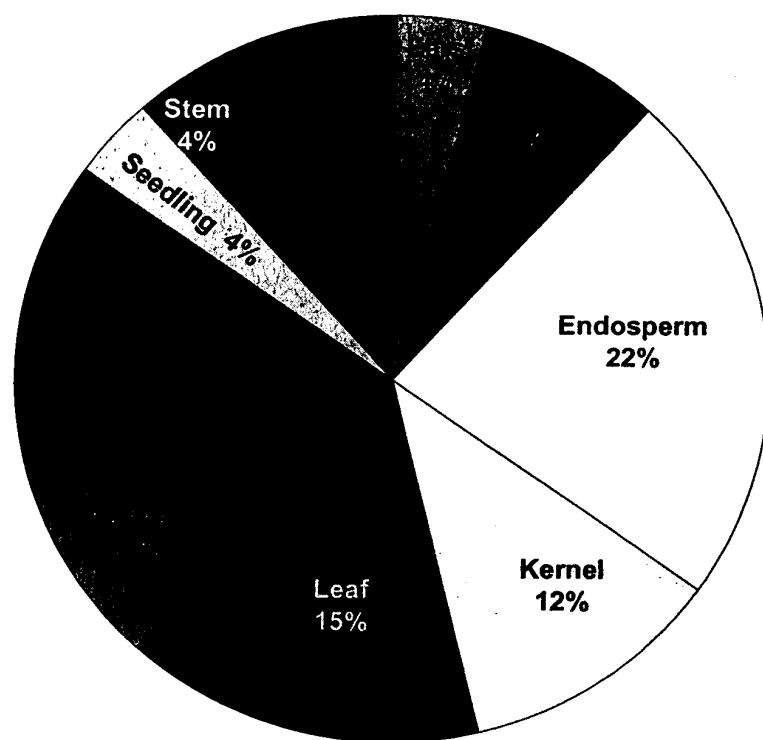


Figure 4.



**Figure 5**

Allele 1: CACCCGG-mu-AGATTG

Allele 2: CACC-mu-CGGAGATTG



Figure 6.



Genotype	structural dry matter (% of total dry matter)	cellulose (% of total dry matter)	cellulose (% of structural dry matter)
<i>Sus-1</i> (WT)	63.2	25.2 +/-0.38	39.9
<i>sus-1</i> (mutant)	47.3	17.7 +/-0.34	37.4

**Figure 7.**

		1		50
Sh1	(1)	----	MAAKLTRLHSLRERLGATFSSHPNELIALFSRYVHQGKGMLOPHQ	
Sus1	(1)		MGEAGADRVLSRLHSVRERIGDLSAHPNELVAVFTRLKNLKGKMLQPHQ	
Sus3	(1)	-----	STHASGDRVEDTLHAHRNELVALLSKYVNVKGGKTLLOPHH	
Consensus	(1)		LSRLHSLRERIGDTLSAHPNELVALFSRYVN GKGMLQPHQ	
		51		100
Sh1	(46)		ILAEDF-AIFDSDKE--KYAPFEDTLRAAQEAMLEPPWVALAIRPRPGVW	
Sus1	(51)		ITAENVNATPEAREKRLKDGAFEDVLRAQENIVLPPWVALAIRPRPGVW	
Sus3	(40)		ILDALDEVQSGGGR-LAEGPFELDLRSAQEAMLEPPWVALAIRPRPGVW	
Consensus	(51)		ILAEDF AI DADRE LKDGPFEDVLRAAQEAVLPPWVALAIRPRPGVW	
		101		150
Sh1	(93)		EYVRVNVSELAVEELSVSEYLAFKEQLVDGQSNFVLELDFEFPNASFP	
Sus1	(101)		EYVRVNVSELAVEELRVPEYLQFKEQLVEGPNNNFVLELDFEFPNASFP	
Sus3	(89)		EYVRVNVSELSVEQLTVSEYLRKEQLVDGQHNDPYVLELDFEFPNASFP	
Consensus	(101)		EYVRVNVSELAVEELSVSEYL FKEQLVDGQ N NFVLELDFEFPNASFP	
		151		200
Sh1	(143)		SSKSKNGVQFLNRHLSSKLFQDKESLYNNRAINYTT	
Sus1	(151)		SSKSKNGVQFLNRHLSSKLFHDKESYNNRAINYMT	
Sus3	(139)		SNRSGNGVQFLNRHLSSKLFIMRNRCLEDDRNRHV	
Consensus	(151)		RPSLSKSGNGVQFLNRHLSSKLF DKESLYPLLNFLRAHNYKG TMLLN	
		201		250
Sh1	(193)		QRRSSRRVLSVPOEENHRLLTK	
Sus1	(201)		RRSSRRVLSVPOEENHRLLCK	
Sus3	(189)		QRRSSRRVLSVPOEENHRLLTK	
Consensus	(201)		DRIQSL ALQSALRKAEEHLSSLPADTPYSEF HRFQELGLEKGGWDTAK	
		251		300
Sh1	(243)		RVLETIHLLDLEAPDPSTLEKFLGTIPMIFNVVILSPHGYFAQANVLG	
Sus1	(251)		RAQETIHLLDLEAPDPSTLEKFLGTIPMIFNVVILSPHGYFAQANVLG	
Sus3	(239)		HVLEMIHLLDLEAPDPSTLEKFLGTIPMIFNVVILSPHGYFAQANVLG	
Consensus	(251)		RVLETIHLLDLEAPDPSTLEKFLGTIPMIFNVVILSPHGYFAQANVLG	
		301		350
Sh1	(293)		YPTGGQVYVYILDQVRALENEMLLRIKQGLDITPKILIVTRLLPDA GT	
Sus1	(301)		YPTGGQVYVYILDQVRAMENEMLLRIKQGLDITPKILIVTRLLPDA GT	
Sus3	(289)		LPDGGQVYVYILDQVRALENEMLLRIKQGLDITPKILIVTRLLPDA GT	
Consensus	(301)		YPTGGQVYVYILDQVRALENEMLLRIKQGLDITPKILIVTRLLPDA GT	
		351		400
Sh1	(343)		TCGQRLKVGTEHTDILRVPPFRNENGILRKWISRFDVWPYLETYTEDVA	
Sus1	(351)		TCGQRLKVGTEHTDILRVPPFRNENGILRKWISRFDVWPYLETYTEDVA	
Sus3	(339)		SCNQRLKVGTEHTDILRVPPFRNENGILRKWISRFDVWPYLETYTEDVA	
Consensus	(351)		TCGQRLKVGTEHTDILRVPPFRNENGILRKWISRFDVWPYLETYTEDVA	
		401		450
Sh1	(393)		SEIMKEMQAKPDLIIGNYSDGNLVATLLAHKMGVTQCTIAHALEKTKYPN	
Sus1	(401)		HEIAGELQANPDLIIGNYSDGNLVACLLAHKMGVTQCTIAHALEKTKYPN	
Sus3	(389)		GEIAELQCTPDFTIIGNYSDGNLVASLLSYKMGITQCTIAHALEKTKYPN	
Consensus	(401)		EIAAELQA PDLIIGNYSDGNLVASLLAHKMGVTQCTIAHALEKTKYPN	
		451		500
Sh1	(443)		SDIYLDKFDSQYHFSCQFTADLIAMNHTDFIITSTFQEIAGSKDTVGQYE	
Sus1	(451)		SDLYWKKFEDHYHFSCQFTTDLIAMNHADFIITSTFQEIAGSKDTVGQYE	
Sus3	(439)		SDIFWKNFDEKYHFSCQFTADIAMNADFIITSTYQEIAGSKDTVGQYE	
Consensus	(451)		SDIYWKKFDD YHFSCQFTADLIAMNHADFIITSTFQEIAGSKDTVGQYE	
		501		550
Sh1	(493)		SHIAFTLPGLYRVVHGIDVFDPKFNIVSPGADMSIYFPYTESKRLTSLH	
Sus1	(501)		SHMAFTMPGLYRVVHGIDVFDPKFNIVSPGADLSIYFPYTESKRLTSLH	
Sus3	(489)		SHIAFTLPGLYRVVHGIDVFDPKFNIVSPGADMSIYFPYTESKRLTSLH	
Consensus	(501)		SHIAFTLPGLYRVVHGIDVFDPKFNIVSPGADMSIYFPYTES KRLTSLH	

Figure 8a



551 600

Sh1 (543) PETEELIYSDVENSEHKFVLKDKKKPTIFSMARLDRVKNMTGLVEMYGKN  
 Sus1 (551) PETEELIYSOTENTEHKFVLNDRNKPTIFSMARLDRVKNLTGLVELYGRN  
 Sus3 (539) GSTENIIMDPEONDEHIGHLDDRSKPIIFSMARLDRVKNMTGLVELYGRN  
 Consensus (551) PETEELIYS ENSEHKFVL DR KPIIFSMARLDRVKNITGLVELYGRN

601 650

Sh1 (593) ARRLRELANLVIVAGDHGK-ESKDREEQAEFKMYSLIDEYKLGHIRWIS  
 Sus1 (601) KRLQELVNLVVVCGDHGN-PSKDKEEQAEFKMYFDLIEQYNLNGHIRWIS  
 Sus3 (589) AKURELVNLVVVAGYNDVNKSKDREEIAEIEKMEELIKTHNIFGQFRWIS  
 Consensus (601) ARRLRELVNLVVVAGDHG SKDREEQAEFKMHDLDID YNL GHIRWIS

651 700

Sh1 (642) AQMNVRVNGELYRYICTDKGAFVQPAFYEAFLTVVEAMTCGLPTIFATCH  
 Sus1 (650) AQMNVRVNGELYRYICTDKGAFVQPAFYEAFLTVVEAMTCGLPTIFATAM  
 Sus3 (639) AQTNVARNGELYRYTADTHGAFVQPALYEAFGLTVVEAMTCGLPTIFATLH  
 Consensus (651) AQMNVRVNGELYRYICTDKGAFVQPAFYEAFLTVVEAMTCGLPTIFAT H

701 750

Sh1 (692) LCPVAVVDLADLPYHSDKIAADLVNEDKKKADSSADEQQG  
 Sus1 (700) LCPVAVVDLADLPYHSDKIAADLVNEDKKKADSSADEQQG  
 Sus3 (689) LCPVAVVDLADLPYHSDKIAADLVNEDKKKADSSADEQQG  
 Consensus (701) GGPAAEIIIVHGVS GFHIDPYH DKAALLVDFFDKCKADPSHW ISQGGL

751 800

Sh1 (742) QRIYKYTWKLYSERLMTLTGVYGFWKYVSNLERRETRYLEM FYALKYR  
 Sus1 (750) QRIYKYTWKLYSERLMTLTGVYGFWKYVSNLERRETRYLEM FYALKYR  
 Sus3 (739) QRIYKYTWKLYSERLMTLTGVYGFWKYVSNLERRETRYLEM FYALKYR  
 Consensus (751) QRIYKYTWKLYSERLMTLTGVYGFWKYVSNLERRETRYLEM FYALKYR

801 817

Sh1 (792) SLASTVPLAID P  
 Sus1 (800) SLASTVPLAID P  
 Sus3 (789) ELKTVPLAID P  
 Consensus (801) SLASTVPLAID P

Figure 8b



### Figure 9b

### Figure 9b

		1051	1100
Sh1	(1040)	TCGATATCACTCCGAAGATCCTCATTGTTACCAGGCTGTTGCTGCTGCTGCTG	
Sus1	(1020)	TGACATCACGCCGAAGATCCTTATTGTCACCAGGTTGCTCCCTGATGCTG	
Sus3	(958)	TCGATGTTTCCCAAAGATTCTCATGCTTACTCCGCTGAAATGAAATG	
Consensus	(1051)	TGATATCAC CCGAAGATCCTCATTGTTACCAGGCTG T CCTGATGCAA	
		1101	1150
Sh1	(1090)	CTGGGACTACGTGCGGTCAGCGGCTGAGAAAGGTCATTGCTAGTGAACAC	
Sus1	(1070)	CTGGCACCACTGTGGCCAGCCCTTGAGAAAGCTCCTTGCCTGCTGCTG	
Sus3	(1008)	AAGGAACATCATGGAATGAGCGGCTTGAGAGAAATAGTGGAAACACGCT	
Consensus	(1101)	CTGG AC AC TCGGTCAGCGGCTTGAGAAGGTCATTGG AC GAGCAC	
		1151	1200
Sh1	(1140)	ACAGACATCAATCGCGTTGCGCTGAGAAATGCTGAAATGCTGCTGCTG	
Sus1	(1120)	TGCCATATTCCTTCGCGTGTGCTGCTGAAACAGAAATCGGATGCTGCTG	
Sus3	(1058)	AGTTACATATTAAGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTG	
Consensus	(1151)	AC ACATC TTCGCGTTCCTTCAGAAATGAAATGG ATCCTTCGCAA	
		1201	1250
Sh1	(1190)	GTGATCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	
Sus1	(1170)	GTGATCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	
Sus3	(1108)	ATGGAATCAAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	
Consensus	(1201)	GTGGATCTC CGATTGATGTCTGGCCATACCTGGAGACATACACTGAGG	
		1251	1300
Sh1	(1240)	ATGTTTTCAGTGAATGAAATGAAATGAAATGAAATGAAATGAAATG	
Sus1	(1220)	ACCTGGGCAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATG	
Sus3	(1158)	ATGCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	
Consensus	(1251)	ATGTTGC GTGAAATTGCTG AGAA T CAGGCCAATCTGACCT ATC	
		1301	1350
Sh1	(1290)	ATTGGCACTACAGCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	
Sus1	(1270)	ATCGGAATCTACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	
Sus3	(1208)	ATTGGCACTACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	
Consensus	(1301)	ATTGGAACTACAGTGATGGAACCTTGT GCGTCTTTGCTCGC CACAA	
		1351	1400
Sh1	(1340)	GTGGGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	
Sus1	(1320)	GATGGGTTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	
Sus3	(1258)	GATGGGAATTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	
Consensus	(1351)	GATGGAGTTACTCAGTGATACCATTGCTCATGC CTGGAGAAAATAAGT	
		1401	1450
Sh1	(1390)	ACCCAACTCGGACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	
Sus1	(1370)	ACCCTAACTCGGACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	
Sus3	(1308)	ATCCAGATTTCAGACATATTTTGGGAAGAAATTTCCGATGAGAGTACCAT	
Consensus	(1401)	ACCC AACTC GACATCTACTGGAAGAA TTCGA GA CAGTACCACTTC	
		1451	1500
Sh1	(1440)	TCTTGCCAGTTCACAGCTGACCTTATTGCTCATGAACCAACCGATTTCAT	
Sus1	(1420)	TCTTGCCAGTTCACCACTGACTTCTATTGCAATGAACCAATGCGGACTTCT	
Sus3	(1358)	TCTTGCCAGTTCAGTCTGATATATTGCTATGAACCAATGCTGATTTTCT	
Consensus	(1451)	TC TGCCAGTTCAC GCTGAC T ATTGC ATGAACCATGCCGATTTCAT	
		1501	1550
Sh1	(1490)	CATCACCAGCACATTCCAAGAAATCGCGGGAAGCAAGGACACCGTGGGG	
Sus1	(1470)	CATCACCAGTACCTTCCAAGAGATCGCGGGAACAAGGACACCGTGGGG	
Sus3	(1408)	CATCACCAGCATACCAAGAAATTCCTGGAAGCAAAAATCTGCTTGGAC	
Consensus	(1501)	CATCACCAGCACATTCCAAGAAATCGC GGAAGCAAGGACACCGT GG C	

**Figure 9c**

1517

		1551	1600
Sh1	(1540)	AGTACGAGTCCATATCGCGTTCACTCTCCTGGGCTCTACCGTGGCTG	
Sus1	(1520)	AGTACGAGTCACACATGGCGTTCAATGCCTGGCCTGTACCGCTGCTG	
Sus3	(1458)	AGTATGAGAGTCATACTGCCITTTACTCTGCCTGGTCTGTACCGAGTGTG	
Consensus	(1551)	AGTACGAGTC CATAT GCGTTCACTCTGCCTGG CTGTACCG GTTGTC	
		1601	1650
Sh1	(1590)	CATGGCATCGATGTTTTCGATCCCAAGTTCAAGATGCTCTCTCTGAGAG	
Sus1	(1570)	CACGGCATTTGATGTGTTTCGACCCCAAGTTCAAGATCCTGCTCTCTGAG	
Sus3	(1508)	CATGGGATCGATGTTTTCGATCCCAAGTTCAAGATGCTCTCTCTGAGAG	
Consensus	(1601)	CATGGCATCGATGT TTCGATCCCAAGTTCAACAT GTCTCTCTGAGAG	
		1651	1700
Sh1	(1640)	AGACATGAGTGTCTTACTACCGTTTATACCGAATCCGAGAGAGAGAGTG	
Sus1	(1620)	GGACCTGTCCATCTACTTCCCGTACCCAGTTCCTCAAGAGAGAGAGAGTG	
Sus3	(1558)	TGACATGTCCATATAATTTTACCTTCCGAGAGAGAGAGAGAGAGAGTG	
Consensus	(1651)	GACATGTCCAT TACTTCCC TATACCGAGACGAGACAAGAGACTCACCT	
		1701	1750
Sh1	(1690)	CGTTCATCTGAAATCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTG	
Sus1	(1670)	CGCTTCCTCGGAGAGTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	
Sus3	(1608)	CTGTTGATGGTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTG	
Consensus	(1701)	CCCTTCATCCTGAAATCGAGGAGCTCAT TACAGCCA G CGAGAAC C	
		1751	1800
Sh1	(1740)	AGGATGAGTGTCTTACTACCGTTTATACCGAATCCGAGAGAGAGAGTG	
Sus1	(1720)	AGGATGAGTGTCTTACTACCGTTTATACCGAATCCGAGAGAGAGAGTG	
Sus3	(1658)	AGGATGAGTGTCTTACTACCGTTTATACCGAATCCGAGAGAGAGAGTG	
Consensus	(1751)	GAGCACAAGTTCGTTCTGAA GACAGGAA AAGCC ATCATCTTCTCCAT	
		1801	1850
Sh1	(1790)	GGCGCGTCTCGACCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	
Sus1	(1770)	GGCTCGTCTCGACCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	
Sus3	(1708)	GGCAAGACTCGACAGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	
Consensus	(1801)	GGC CGTCTCGACCG GTGAAGAACATGACAGGGCTGGTTCGAG TGTACG	
		1851	1900
Sh1	(1840)	GCAAGAACGCGCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	
Sus1	(1820)	GCCGGAAGAACGCGGTGCAAGCTTCTCTCTCTCTCTCTCTCTCTCTCTCT	
Sus3	(1758)	CTAAGTGGCTAAGCTGAGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	
Consensus	(1851)	GCAAGAACGCGCGGCTGAGGGAGCTGGTGAACCTCGTGGTCTGTCGCGG	
		1901	1950
Sh1	(1890)	GACCATGG ---CAAGGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	
Sus1	(1870)	GACCATGG ---CAACCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	
Sus3	(1808)	TACAATGATGTCAACAAGTCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG	
Consensus	(1901)	GACCATGG CAAC AGTCCAAGGACAGGGAGGAGCAGGCGGAGTTCAA	
		1951	2000
Sh1	(1937)	GAAGATGTACAGCCTCATCGAGAGTACAAAGAGAGAGAGAGAGAGAGAG	
Sus1	(1917)	GAAGATGTTTACCTCATCGAGAGTACAAAGAGAGAGAGAGAGAGAGAGAG	
Sus3	(1858)	GAAGATGATGAATCATCAAGACCCACAACCTTCTCTCTCTCTCTCTCTCT	
Consensus	(1951)	GAAGATGTATGACCTCATCGAG AGTACAACCTTGAACGGGCA ATCCGCT	
		2001	2050
Sh1	(1987)	GGATCTCGGCGCAGATGAACCGTGTCCGCAACGGGAGAGAGAGAGAGAG	
Sus1	(1967)	GGATCTCGGCGCAGATGAACCGTGTCCGCAACGGGAGAGAGAGAGAGAGAG	
Sus3	(1908)	GGATCTCTGCCCAGACAAACAGGCCCCTAAGGGGAGAGAGAGAGAGAGAG	
Consensus	(2001)	GGATCTC GCCAGATGAACCG GTCCGCAACGGGAGCTGTACCGCTAC	
		2051	2100
Sh1	(2037)	ATTTGCGATACCAAGGGCGCATTCGTGCAGCCTGCGTTCTACGAAGCGTT	
Sus1	(2017)	ATCTGCGACACCAAGGGCGCTTCGTGCAGCCTGCTTTCTACGAGGCTTT	
Sus3	(1958)	ATCGCTGATACCATGGTGCTTTCTGTACAGCCGGCCTTGATGAAGCGTT	
Consensus	(2051)	ATCTGCGATACCAAGGGCGC TTCGTGCAGCCTGC TTCTACGAAGCGTT	

Figure 9d

2101 2150

Sh1 (2087) CGGCCTGACTGTGATCGAGTCCATGACGTGCGGTCTGCCAAGGAGCGG

Sus1 (2067) CGGGCTGACGGTGGTTGAGGCCATGACCTGCGGCCTGCCACCGTGGG

Sus3 (2008) CGGTCTCACCCTCGTTGAGGCCATGACCTGTGGGTTGGTCTGTT

Consensus (2101) CGG CTGAC GTGGTTGAGGCCATGACCTGCGG CTGCC ACGTTCGCGA

2151 2200

Sh1 (2137) CCTGCCATGGCGGCCCTGCTGAGATCATGCTGACGGGGTATCTGGCC

Sus1 (2117) CCGCCTACCGCGGTTCCGGCCGAGATGATGCTGACCGCGTGTCTGATAT

Sus3 (2058) CGCTCCATGGAGGTCCAGCTGACATCATAGACCTGGCGTCTGGTGGATC

Consensus (2151) CC CCATGGCGGTCC GCTGAGATCATCGTGACGGCGT TCTGGCTTC

2201 2250

Sh1 (2187) CACATTGACCCCTTACCACAGCGACAAGGCCTCGGATATCTGCTG

Sus1 (2167) CACATCGACCCCTTACCAGGGCGACAAGGCGTGGGCCCTGCTCG

Sus3 (2108) CACATTGACCCCTTACCACCCGACAGGCTGTTAATCTGAGCTCG

Consensus (2201) CACATTGACCCCTTACCAC GCGACAAGGC GCGGATCTGCTGGTTCGACTT

2251 2300

Sh1 (2237) CTTCGACAAGTGCAAGGCAGA CCGAGCCACTGGG CAAGATCTC CAGG

Sus1 (2217) CTTCGACAAGTGCAAGGCAGA CCGAGCCACTGGG CAAGATCTC CAGG

Sus3 (2158) CTTCGACAAGTGCAAGGCAGA CCGAGCCACTGGG CAAGATCTC CAGG

Consensus (2251) CTTCGACAAGTGCAAGGCAGA CCGAGCCACTGGG CAAGATCTC CAGG

2301 2350

Sh1 (2287) GCGGGCTGCAGCG AT TA GAGAAGTACACCTGGAAGCT TACTC GAG

Sus1 (2267) GCGGGCTGCAGCG AT TA GAGAAGTACACCTGGAAGCT TACTC GAG

Sus3 (2208) GCGGGCTGCAGCG AT TA GAGAAGTACACCTGGAAGCT TACTC GAG

Consensus (2301) GCGGGCTGCAGCG AT TA GAGAAGTACACCTGGAAGCT TACTC GAG

2351 2400

Sh1 (2337) AGGCTGATGACCCTGACCGGCGTGTACGGGTTCTGGAAGTACGTGCCAA

Sus1 (2317) AGGCTGATGACCCTGACCGGCGTGTACGGGTTCTGGAAGTACGTGCCAA

Sus3 (2258) AGGCTGATGACCCTGACCGGCGTGTACGGGTTCTGGAAGTACGTGCCAA

Consensus (2351) AGGCTGATGACCCTGACCGGCGTGTACGGGTTCTGGAAGTACGTGCCAA

2401 2450

Sh1 (2387) CCTGGAGAGGCGCGAGACCCGCGCTACCT GAGATGTTCTACGC CTGA

Sus1 (2367) CCTGGAGAGGCGCGAGACCCGCGCTACCT GAGATGTTCTACGC CTGA

Sus3 (2308) CCTGGAGAGGCGCGAGACCCGCGCTACCT GAGATGTTCTACGC CTGA

Consensus (2401) CCTGGAGAGGCGCGAGACCCGCGCTACCT GAGATGTTCTACGC CTGA

2451 2500

Sh1 (2437) AGTACCGCA CCTGGCGAGCACCGTGCCGCTGGCC T GA G AG

Sus1 (2417) AGTACCGCA CCTGGCGAGCACCGTGCCGCTGGCC T GA G AG

Sus3 (2358) AGTACCGCA CCTGGCGAGCACCGTGCCGCTGGCC T GA G AG

Consensus (2451) AGTACCGCA CCTGGCGAGCACCGTGCCGCTGGCC T GA G AG

2501 2550

Sh1 (2481) TACGGGGAAAGAAAGGAGA-AGAAGAAAGAGAAGCCAGGGCGGA

Sus1 (2461) TACGGGGAAAGAAAGGAGA-AGAAGAAAGAGAAGCCAGGGCGGA

Sus3 (2408) TACGGGGAAAGAAAGGAGA-AGAAGAAAGAGAAGCCAGGGCGGA

Consensus (2501) TAGC GC AGAA G GA TGCCTAACA GGCACAGGCCTGA G

2551 2600

Sh1 (2525) AACCATCGCCTGCATTTCGATCT-----GT-TTCAACCGCAATTGGC

Sus1 (2507) AACCATCGCCTGCATTTCGATCT-----GT-TTCAACCGCAATTGGC

Sus3 (2458) AACCATCGCCTGCATTTCGATCT-----GT-TTCAACCGCAATTGGC

Consensus (2551) AACCATCGCCTGCATTTCGATCT-----GT-TTCAACCGCAATTGGC

Figure 9e



CGCCAGTCGCCAGTCGCCACAGCCACACCACACCACACTAGCCGCGGCCGCGGGTAGGAG  
CGCGCGCGGGCGCGGCGGAACGACCCACCGGTGGCGGCAGCCATGTCTGCCCCGAAGCTGA  
ACCGCAACGCGAGCATCCGGGACCGCGTCGAGGACACCCTCCACGCGCACCGCAACGAGC  
TCGTCGCCCTCCTCTCCAAGTACGTGAACAAGGGGAAGGGCATCCTGCAGCCGCACCACA  
TCCTCGACGCGCTCGACGAGGTCCAGGGCTCCGGGGTCCGCGCGCTCGCCGAGGGACCCCT  
TCCTCGACGTCCTCCGCTCCGCGCAGGAGGCGATCGTGCTGCCGCCG

**Figure 10**



**Sorghum sequence from SEQ ID NO: 13 in SEQ ID NO: 11**  
 ATGTCTGCCCGAAGCTGAACCGCAACGCGAGCATCCGG

**Maize sequence from SEQ ID NO: 1 in SEQ ID NO: 11**

accgcgctcga	ggacaccctc	cacgcgacc	gcaacgagct	60
cgctgcacctc	ctgtccaagt	acgtgaacaa	gggaagggc	120
cctcgacgag	ctcgacgagg	tccagggctc	cggggggccg	180
cctcgacgctc	ctccgctccg	cgcaggaggc	gatcgtgctg	240
ggtgcgcccg	cgcccgggag	tttgggagta	cgcccgctc	300
cgagcagctc	acagtctcgg	agtacctccg	cttcaaggag	360
caatgatccc	tacgtttctc	agcttgactt	cgagccgttc	420
aaatcggtca	tcatctattg	gaaacgggtg	gcagttcttc	480
catgttccgc	aacagggtat	gcttggagcc	cctgttggat	540
caaggggcat	gttatgatgc	ttaatgatag	aatacaaaagc	600
gctgaccaaa	gctgaggagc	acttgtcaaa	gctccctgct	660
tgtttataaa	tttcaagagt	ggggcctgga	gaaagggttg	720
tttggaagt	atccatctcc	ttctagacat	cattcaggcg	780
gaaattcttg	gggaggatcc	ccatgatttt	taacgtttgt	840
ctttggtcaa	gctaattgat	taggcttgcc	agacacagga	900
ggaccaagtc	cgtgcactag	aaaatgagat	ggttctccgt	960
tgtttcccca	aagatttctc	ttgttactcg	gctgatacca	1020
caatcagcgg	cttgagagaa	ttagtggaac	acagcatact	1080
cagaaatgaa	aatgggatac	ttaagaaatg	gatatcaaga	1140
ggaaacattt	gctgaggatg	ctgctgggta	aattgctgct	1200
cttcataatt	ggaaactaca	gtgatggaaa	tcttggtggc	1260
gggaattacc	cagtgcacaa	ttgctcatgc	tctggaaaag	1320
catatttttg	aagaatttct	atgagaagta	ccatttctcc	1380
aattgctatg	aacaatgctg	attttatcat	caccagcaca	1440
caaaaatact	ggttgacagt	atgagagtca	tactgccttt	1500
agttgtccat	gggatcgatg	tcttcgatcc	aaagtccaat	1560
catgtccata	tactttccac	ataccgagaa	ggccaagcga	1620
aatcgaaaat	ttgatttatg	acccgagaca	aaacgatgaa	1680
ccggtcaaa	cccatctctc	tctccatggc	aagactcgac	1740
gctggtcgaa	gcttttgcta	agtgcgctaa	gctgagggag	1800
tgccgggtac	aatgatgtca	acaagtccaa	ggacagggaa	1860
gatgcatgaa	ctcatcaaga	cccacaactt	gttcggggag	1920
gacaaacagg	gcccgtaacg	gcgagctcta	tcgtacatc	1980
cgtacagccg	gccttgatat	aagcgttcgg	tctcacccgc	2040
gcttctact	ttcgcgacgc	tccatggagg	tccagctgag	2100
gggcttccac	attgaccggt	accaccccga	acaggctgtt	2160
cgaccggtgc	aagcaagacc	cagatcactg	ggtgaatata	2220
catatacgag	aagtacacat	ggaagatata	ctcagagagg	2280
ctacgggttc	tggaaagtacg	tgtcgaagct	cgagaggctg	2340
gatgttctac	atactgaagt	tccgcgagct	ggcgaagacc	2400
accgcagtag	cttgcgcaac	tgcgactcg	tagcacttgg	2460
gaccttcagt	aatttaggcg	cggcagacgg	tagccaataa	2520
gttttttatt	atgtacataa	tggcagatata	acaaaattac	2580
ttgtgtgttc	gttactgttt	actgtattat	gtcaagctgt	2640
gcaagccgca	ggcactggtg	aagtgtctgat	aaatacatca	2700
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaag	cgccgcgc	

**Figure 11**